Title: GENES RESPONSIBLE FOR
VERNALIZATION REGULATION IN
TEMPERATE GRASSES AND USES THEREOF
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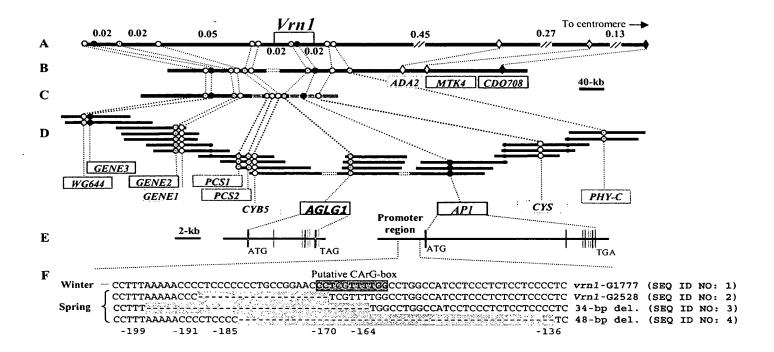Filed: **Concurrently Herewith**
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Fig. 1

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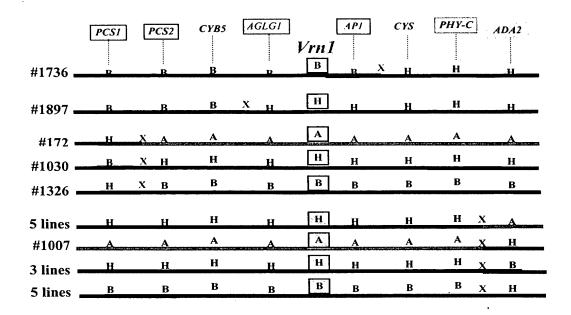Docket No.: **514112000320 Sheet 2 of 21**

Figure 2A

Figure 2B

F_2 family	G2528	G1777	AA		AB		BB	
			N	D	N	D	N	D
#1736	0 D	45 D	10	-5/+1	16	-5/0	10	-5/+1
#1897	0 D	60 D	7	35/40	22	-5/0	8	-5/0

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Figure 3

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Figure 4

A.

B.

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Figure 5

Ap1 transcription in leaves of different ag_

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Figure 6

#sf 1470122

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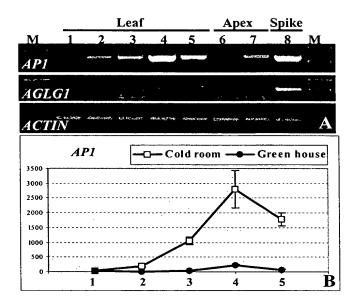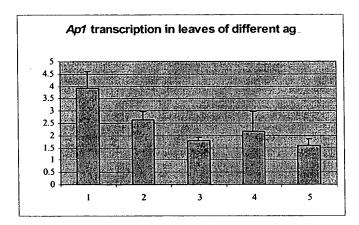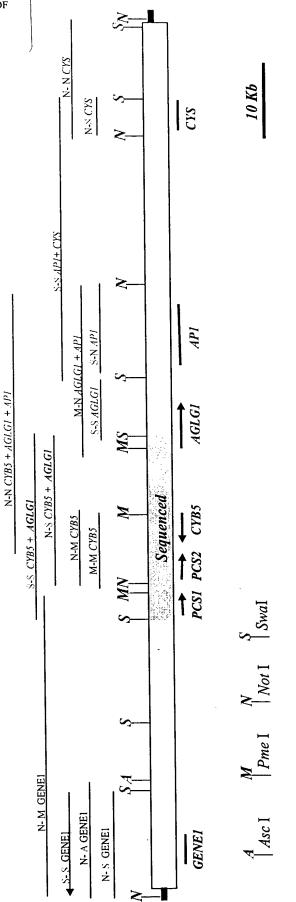Docket No.: **514112000320 Sheet 7 of 21**

Figure 7

G2528 (*Vrn1*) = DV92 (*vrn1*)

A. ATGGGGCGCGGGAAGGTGCAGCTGAAGCGGATCGAGAACAAGATCAACCGGCAGGTGACCTTCTCCAAG
CGCCGCTCGGGGCTTCTCAAGAAGGCGCACGAGATCTCCGTGCTCTGCGACGCCGAGGTCGGCCTCATC
ATCTTCTCCACCAAGGGGAAAGCTCTACGAGTTCTCCACCGAGTCATGTATGGACAAAATTCTTGAACGG
TATGAGCGCTATTCTTATGCAGAAAAGGTTCTCGTTTCAAGTGAATCTGAAATTCAGGGAAACTGGTGT
CACGAATATAGGAAACTGAAGGCGAAGGTTGAGACAATACAGAAATGTCAAAAACATCTCATGGGAGAG
GATCTTGAATCTTTGAATCTCAAGGAGTTGCAGCAACTGGAGCAGCAGCTGGAAAGCTCACTGAAACAT
ATCAGATCCAGGAAGAACCAACTTATGCACG<u>A</u>ATCCATTTCTGAGCTGCAGAAGAAGGAGAGGTCACTG
CAGGAGGAGAATAAAGTTCTCCAGAAGGAACTCGTGGAGAAGCAGAAGGCCCATGCGGCGCAGCAAGAT
CAAACTCAGCCTCAAACCAGCTCTTCTTCTTCCTTCATGCTGAGGGATGCTCCCCCTGCCGCAAAT
ACCAGCATTCATCCAGCGGCGGCAGGCGAGAGGGCAGAGGATGCGGCAGTGCAGCCGCAGGCCCCACCC
CGGACGGGGCTTCCACCGTGGATGGTGAGCCACATCAACGGG**TGA** (SEQ ID NO: 5)

B. G1777 (*vrn1*) = G3116(*vrn1*)

ATGGGGCGCGGGAAGGTGCAGCTGAAGCGGATCGAGAACAAGATCAACCGGCAGGTGACCTTCTCCAAG
CGCCGCTCGGGGCTTCTCAAGAAGGCGCACGAGATCTCCGTGCTCTGCGACGCCGAGGTCGGCCTCATC
ATCTTCTCCACCAAGGGGAAAGCTCTACGAGTTCTCCACCGAGTCATGTATGGACAAAATTCTTGAACGG
TATGAGCGCTATTCTTATGCAGAAAAGGTTCTCGTTTCAAGTGAATCTGAAATTCAGGGAAACTGGTGT
CACGAATATAGGAAACTGAAGGCGAAGGTTGAGACAATACAGAAATGTCAAAAACATCTCATGGGAGAG
GATCTTGAATCTTTGAATCTCAAGGAGTTGCAGCAACTGGAGCAGCAGCTGGAAAGCTCACTGAAACAT
ATCAGATCCAGGAAGAACCAACTTATGCAG<u>G</u>ATCCATTTCTGAGCTGCAGAAGAAGGAGAGGTCACTGC
AGGAGGAGAATAAAGTTCTCCAGAAGGAACTCGTGGAGAAGCAGAAGGCCCATGCGGCGCAGCAAGATC
AAACTCAGCCTCAAACCAGCTCTTCTTCTTCCTTCATGCTGAGGGATGCTCCCCCTGCCGCAAATA
CCAGCATTCATCCAGCGGCGGCAGGCGAGAGGGCAGAGGATGCGGCAGTGCAGCCGCAGGCCCCACCCC
GGACGGGGCTTCCACCGTGGATGGTGAGCCACATCAACGGG**TGA** (SEQ ID NO: 6)

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Figure 8

A. G2528 (*Vrn1*) = DV92 (*vrn1*)
MGRGKVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIIFSTKGKLYEFSTESCMDKILERYER
YSYAEKVLVSSESEIQGNWCHEYRKLKAKVETIQKCQKHLMGEDLESLNLKELQQLEQQLESSLKHIRSR

KNQLMH**E**SISELQKKERSLQEENKVLQKELVEKQKAHAAQQDQTQPQTSSSSSSFMLRDAPPAANTSIHP
AAAGERAEDAAVQPQAPPRTGLPPWMVSHING* (SEQ ID NO: 7)

B. G1777 (*vrn1*) = G3116(*vrn1*)
MGRGKVQLKRIENKINRQVTFSKRRSGLLKKAHEISVLCDAEVGLIIFSTKGKLYEFSTESCMDKILERYER
YSYAEKVLVSSESEIQGNWCHEYRKLKAKVETIQKCQKHLMGEDLESLNLKELQQLEQQLESSLKHIRSR

KNQLMH**G**SISELQKKERSLQEENKVLQKELVEKQKAHAAQQDQTQPQTSSSSSSFMLRDAPPAANTSIHP
AAAGERAEDAAVQPQAPPRTGLPPWMVSHING* (SEQ ID NO. 8)

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Figure 9A

```
G2528     1  ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
DV92      1  ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
G1777     1  ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC
G3116     1  ATTTGCCTGATGAGACGCTTGACAACAGTGTATTGATGGATGTCTGGTCGGTATACACGC

G2528    61  ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTCATTCCAGAAATACG
DV92     61  ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTCATTCCAGAAATACG
G1777    61  ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTCATTCCAGAAATACG
G3116    61  ACAGCACAGTACCCCTACTCCTAGGACTGGCGAGTATCTTTCATTCATTCCAGAAATACG

G2528   121  CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGCAGCGCACTGCAC
DV92    121  CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGCAGCGCACTGCAC
G1777   121  CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGTAGCGCACTGCAC
G3116   121  CGGGTCGGCCAAAAGTAGAAAAATACACTGCGCCCACTCAATCCACGTAGCGCACTGCAC

G2528   181  TGCACAGCAACGCTTCATGTCAAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
DV92    181  TGCACAGCAACGCTTCATGTCAAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
G1777   181  TGCACAGCAACGCTTCATGTCAAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC
G3116   181  TGCACAGCAACGCTTCATGTCAAAAGTCGAGCTCAAGCATGCACGCGATGGACGCGGCGC

G2528   241  GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCCTGCCCCGCAGCCG
DV92    241  GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCCTGCCCCGCAGCCG
G1777   241  GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCCTGCCCCGCAGCCG
G3116   241  GAATGACCCGGGCGGCACGACGCGAGTGCCCGCCGCGCCCGCCCGCCTGCCCCGCAGCCG

G2528   301  ACCTCTTCCCAAACGGGACAAGCGAGACGGCCCAAAACGAGCAAGGAAAGCAGCCTCCTA
DV92    301  ACCTCT-CCCAAACGGGACAAGCGAGACGGCCCAAAACGAGCAAGGAAAGCAGCCTCCTA
G1777   301  ACCTCT-CCCAAACGGGACAAGCGAGACGGCCCAAAACGAGCAAGGAAAGCAGCCTCCTA
G3116   301  ACCTCT-CCCAAACGGGACAAGCGAGACGGCCCAAAACGAGCAAGGAAAGCAGCCTCCTA

G2528   361  CTGTGGCAGCCCGCCCCCACGACCGTCATCTCGCCTTCCATTCCATTTTCCCTGGACGGA
DV92    360  CTGTGGCAGCCCGCCCCCACGACCGTCATCTCGCCTTCCATTCCATTTTCCCTGGACGGA
G1777   360  CTGTGGCAGCCCGCCCCCACGACCGTCATCTCACCCTCCATTCCATTTTCCCTGGACGGA
G3116   360  CTGTGGCAGCCCGCCCCCACGACCGTCATCTCACCTTCCATTCCATTTTCCCTGGACGGA

G2528   421  CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCCTCTTTCGTCCCCCGCC
DV92    420  CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCCTCTTTCGTCCCCCGCC
G1777   420  CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCCTCTTTCGTCCCCCGCC
G3116   420  CCAGACCCGTCCGAGCCGCCCTGACCTAGCCAGCCAGCATTTCCTCTTTCGTCCCCCGCC

G2528   481  GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAATGCTAAAGGAAAAAACTCCGCTC
DV92    480  GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAATGCTAAAGGAAAAAACTCCGCTC
G1777   480  GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAATGCTAAAGGAAAAAACTCCGCTC
G3116   480  GCCGTGACCAAAAAAGCAAAAAAGGAAAAAGGGAAAATGCTAAAGGAAAAAACTCCGCTC

G2528   541  TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTCTGCTCGT
DV92    540  TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTCTGCTCGT
G1777   540  TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTCTGCTCGT
G3116   540  TTTCCCTTCTTCTAGGCCTAGGGTACAGTAGAATATTATAAAAGGAAAAATTCTGCTCGT

G2528   601  TTTTTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAATGATTTGGGGAAAGCAAAATCGG
DV92    600  TTTTTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAATGATTTGGGGAAAGCAAAATCGG
G1777   600  TTTTTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAATGATTTGGGGAAAGCAAAATCGG
G3116   600  TTTTTGCTCTGTGGTGTGTGTTTGTGGCGAGAGAAAATGATTTGGGGAAAGCAAAATCGG

G2528   661  GAGATTCGCACGTACGATCGTTCGACACGTCGACGCCCGGCGGGCCCGTGGTGGGGCATC
DV92    660  GAGATTCGCACGTACGATCGTTCGACACGTCGACGCCCGGCGGGCCCGTGGTGGGGCATC
G1777   660  GAGATTCGCACGTACGATCGTTCGACACGTCGACGCCCGGCGGGCCCGTGGTGGGGCATC
G3116   660  GAGATTCGCACGTACGATCGTTCGACACGTCGACGCCCGGCGGGCCCGTGGTGGGGCATC
```

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Figure 9B

```
G2528   721  GTGTGGCTGCAGGACCGCGGGGCCCCGCGGGGCGGGCCGGGCCAATGGGTGCTCGACAGC
DV92    720  GTGTGGCTGCAGGACCGCGGGGCCCCGCGGGGCGGGCCGGGCCAATGGGTGCTCGACAGC
G1777   720  GTGTGGCTGCAGGACCGCGGGGCCCCGCGGGGCGGGCCGGGCCAATGGGTGCTCGACAGC
G3116   720  GTGTGGCTGCAGGACCGCGGGGCCCCGCGGGGCGGGCCGGGCCAATGGGTGCTCGACAGC

G2528   781  GGCTATGCTCCAGACCAGCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
DV92    780  GGCTATGCTCCAGACCAGCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
G1777   780  GGCTATGCTCCAGACCAGCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA
G3116   780  GGCTATGCTCCAGACCAGCCCGGTATTGCATACCGCGCTCGGGGCCAGATCCCTTTAAAA

G2528   841  ACCC-------------------TCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
DV92    840  ACCCCTCCCCCCCTGCCGGAACCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
G1777   840  ACCCCTCCCCCCCTGCCGGAACCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC
G3116   840  ACCCCTCCCCCCCTGCCGGAACCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTC

G2528   881  TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
DV92    900  TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
G1777   900  TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC
G3116   900  TCTTCCACCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGC

G2528   941  CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCG
DV92    960  CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCG
G1777   960  CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCG
G3116   960  CAGTCGGAGTAGCCGTCGCGGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCG

G2528  1001  GTTCTCGAGCGGAGATG  Start codon (SEQ ID NO: 9)
DV92   1020  GTTCTCGAGCGGAGATG  Start codon (SEQ ID NO: 10)
G1777  1020  GTTCTCGAGCGGAGATG  Start codon (SEQ ID NO: 11)
G3116  1020  GTTCTCGAGCGGAGATG  Start codon (SEQ ID NO: 12)
```
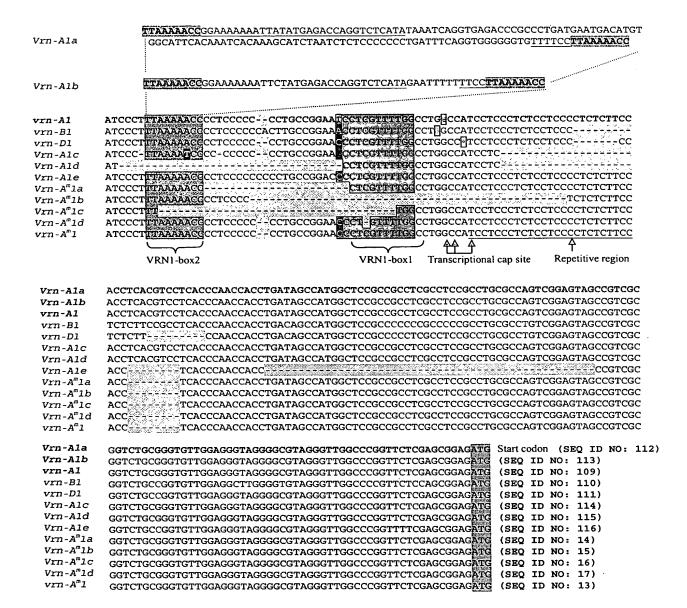
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Figure 10

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Figure 11

```
Vrn-A1a   TTAAAAACCGGAAAAAAATTATATGAGACCAGGTCTCATATAAATCAGGTGAGACCCGCCCTGATGAATGACATGT
          GGCATTCACAAATCACAAAGCATCTAATCTCTCCCCCCCTGATTTCAGGTGGGGGGTGTTTTCCTTAAAAACC


Vrn-A1b   TTAAAAACCGGAAAAAAATTCTATGAGACCAGGTCTCATAGAATTTTTTTCCTTAAAAACC


vrn-A1    ATCCCTTTAAAAACCCCTCCCCC--CCTGCCGGAATCCTCGTTTTGGCCTGCCATCCTCCCTCTCCTCCCCTCTCTTCC
vrn-B1    ATCCCTTTAAAAACGCCTCCCCCCACTTGCCGGAAAGGTCGTTTTGGCCTGCCATCCTCCCTCTCCTCCC----------
vrn-D1    ATCCCTTTAAAAACCCCTCCCCC--CCTGCCGGAACCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCC--------CC
Vrn-A1c   ATCCC-TTAAAATCCCC-CCCCC--CCTGCCGGAAGCCTCGTTTTGGCCTGGCCATCCTC---------------------
Vrn-A1d   AT------------------------------CCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
Vrn-A1e   ATCCCTTTAAAAACCCCTCCCCCCCCCTGCGGACCCCTCGGTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
Vrn-Aᵐ1a  ATCCCTTTAAAAACC----------------CTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
Vrn-Aᵐ1b  ATCCCTTTAAAAACGCCTCCCC------------------------------TCTCTCTTCC
Vrn-Aᵐ1c  ATCCCTT------------------------------CCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
Vrn-Aᵐ1d  ATCCCTTTAAAAACCCCTCCCCC--CCTGCCGGAAGCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
vrn-Aᵐ1   ATCCCTTTAAAAACCCCTCCCCC--CCTGCCGGAACCCTCGTTTTGGCCTGGCCATCCTCCCTCTCCTCCCCTCTCTTCC
```

VRN1-box2   VRN1-box1   Transcriptional cap site   Repetitive region

```
Vrn-A1a   ACCTCACGTCCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-A1b   ACCTCACGTCCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
vrn-A1    ACCTCACGTCCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
vrn-B1    TCTCTTCCGCCTCACCCAACCACCTGACAGCCATGGCTCCGCCCCCCGCCCCCGCCTGCGCCTGTCGGAGTAGCCGTCGC
vrn-D1    TCTCTT----------CCAACCACCTGACAGCCATGGCTCCGCCCCCCTCGCCTCCGCCTGCGCCTGTCGGCGGAGTAGCCGTCGC
Vrn-A1c   ACCTCACGTCCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-A1d   ACCTCACGTCCTCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-A1e   ACC--------TCACCCAACCACC------------------------------------------CCGTCGC
Vrn-Aᵐ1a  ACC--------TCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-Aᵐ1b  ACC--------TCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-Aᵐ1c  ACC--------TCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
Vrn-Aᵐ1d  ACC--------TCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
vrn-Aᵐ1   ACC--------TCACCCAACCACCTGATAGCCATGGCTCCGCCGCCTCGCCTCCGCCTGCGCCAGTCGGAGTAGCCGTCGC
```

```
Vrn-A1a   GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  Start codon  (SEQ ID NO: 112)
Vrn-A1b   GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 113)
vrn-A1    GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 109)
vrn-B1    GGTCTGCCGGTGTTGGAGGCTTGGGGTGTAGGGTTGGCCCCGTTCTCCAGCGGAGATG  (SEQ ID NO: 110)
vrn-D1    GGTCTGCCGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 111)
Vrn-A1c   GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 114)
Vrn-A1d   GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 115)
Vrn-A1e   GGTCTGCCGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTTTCGAGCGGAGATG  (SEQ ID NO: 116)
Vrn-Aᵐ1a  GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 14)
Vrn-Aᵐ1b  GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 15)
Vrn-Aᵐ1c  GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 16)
Vrn-Aᵐ1d  GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 17)
vrn-Aᵐ1   GGTCTGCGGGTGTTGGAGGGTAGGGGCGTAGGGTTGGCCCGGTTCTCGAGCGGAGATG  (SEQ ID NO: 13)
```

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Figure 12

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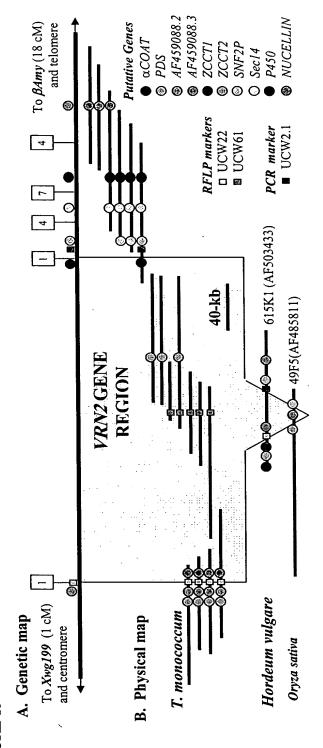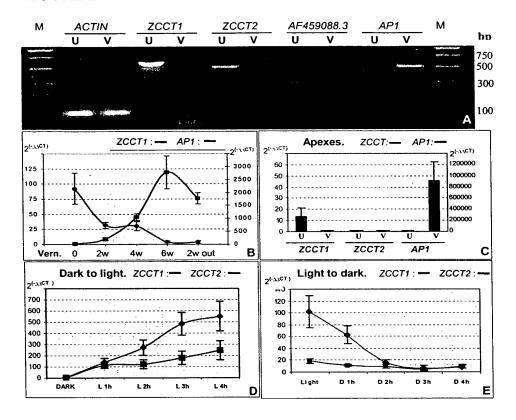Docket No.: 514112000320 Sheet 14 of 21

FIGURE 13
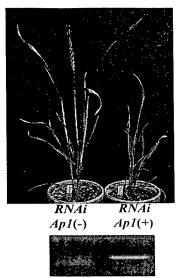
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FIGURE 14

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FIGURE 15A

Transgenic Jagger cDNAs

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FIGURE 15B

RNAi   RNAi
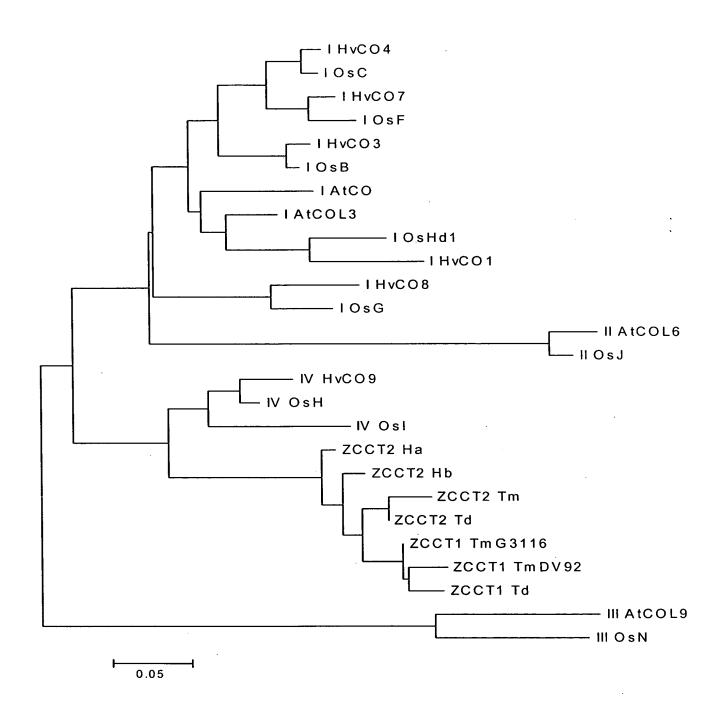*Ap1*(-)   *Ap1*(+)

Transgenic Bobwhite cDNAs

FIGURE 15C

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FIGURE 16

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FIGURE 17

ZCCT1 in leaves.   Long day: ———   Continuous light: ▬ ▬

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FIGURE 18

A

ZCCT1_TmDV92	ER AKVMRYREKRKRRRYDKQIRYESRKAYAE RP VNGRFVKV	(SEQ ID NO: 117)
ZCCT1_TmG3116	ER AKVMRYREKRKRRRYDKQIRYESRKAYAE RPRVNGRFVKV	(SEQ ID NO: 118)
ZCCT1_Td	ER AKVMRYREKRKRRRYDKQIRYESRKAYAE RPRVNG FVKV	(SEQ ID NO: 119)
ZCCT2_Tm	EREAKVMRYREKRKRR YDKQIRYESRKAYAE RPRVNG FVKV	(SEQ ID NO: 120)
ZCCT2_Td	EREAKVMRYREKRKRR YDKQIRYESRKAYAE RPRVNGRFVKV	(SEQ ID NO: 121)
ZCCT2_Hb(Fan)	EREAKVMRYREKRKKRRYDKQIRYESRKAYAE RPRVNGRFVKV	(SEQ ID NO: 122)
ZCCT2_Ha	EREAKVMRYREKRKRRRYDKQIRYESRKAYAE RPRVNGRF KV ZCCT	(SEQ ID NO: 123)
OsI	EREAK MRY EKRKKR YEKQIRY SRKAYAE RPRV GRFAK	(SEQ ID NO: 124)
HvCO9	REAK MRY EKRKRRRY KQIRY SRKAYAE RPRV KGRFAKV	(SEQ ID NO: 125)
OsH	REAKVMRY EKRKRRRY KQIRY SRKAYAE RPRV KGRFAKV Group IV	(SEQ ID NO: 126)
AtCO	REA V RYREKRK RKEEK IRY SRKAYAE RPRVNGRF KR	(SEQ ID NO: 127)
OsHd1	REA V RYREKKAR K EK IRYE RKAYAE RPRE GRF KR	(SEQ ID NO: 128)
HvCO1	EREARV RY EKKK RK EK KT RY RKAYAE ARPRE GRF KR Group Ia	(SEQ ID NO: 129)
HvCO3	REARV RYREKRK RREEK IRY SRKAYAE RPRE GRF KR	(SEQ ID NO: 130)
OsB	REAKV RYREKRK RREEK IRY SRKAYAE RPRE GRF KR Group Ib	(SEQ ID NO: 131)
HvCO4	EREAR MRYREKRK RREEK IRY SRKAYAE RPRV GRF KR	(SEQ ID NO: 132)
OsC	EREAR MRYREKRK RRE EK IRY SRKAYAE RPRE GRF KR	(SEQ ID NO: 133)
AtCOL3	EREAKV RYREKRK RK DK IRY SRKAYAE RPRE GRFAK R Group Ic	(SEQ ID NO: 134)
HvCO7	GREAR MRYREKRK RRE K IRY SRKAYAE RPRV GRF KR	(SEQ ID NO: 135)
OsF	GR AK MRYREKRK RRE K IRY SRKAYAE RPRV KGRFAKR Group Id	(SEQ ID NO: 136)
HvCO8	D AARVMRYREKRK RK HK IRY SRKAYAE ARPRE GRFVKR	(SEQ ID NO: 137)
OsG	RE RVMRYREKRK RK HK IRY SRKAYAE ARPRE GRFVK Group Ie	(SEQ ID NO: 138)
AtCOL6	GREAR VSRYREKR TRL SKK IRYEV RK NAE RPRMKGRFVKR	(SEQ ID NO: 139)
OsJ	EREA VSRYREKR TRL AKK IRYEV RK NAE RPRMKGRFVK Group II	(SEQ ID NO: 140)
AtCOL9	RNNAVMRY EKKKARK DKRVRY SRKA AD RRRV GRFVKA	(SEQ ID NO: 141)
OsN	SRDNA RY EKKKRRK DK IRY SRKA ADVRKRV GRFVKA Group III	(SEQ ID NO: 142)

Tm=*T. monococcum*, Td=*T. dicoccoides* A genome, Hv=*Hordeum vulgare*, Os=*O. sativa*.

Title: GENES RESPONSIBLE FOR
VERNALIZATION REGULATION IN
TEMPERATE GRASSES AND USES THEREOF
Appln. No: **Not Yet Assigned**
Filed: **Concurrently Herewith**
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FIGURE 18

B

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ZCCT1_Td_A       MSMSCGLCGANNCPRLMVSPIHHHHHHHQEHQL Hx₃H position not certain
                                                   (SEQ ID NO: 143)
ZCCT1_DV92       MSMSCGLCGANNCPRLMVSPIHHHHHHHQEHQL Hx₃H position not certain
                                                   (SEQ ID NO: 144)
ZCCT1_G3116      MSMSCGLCGANNCPRLMVSPIHHHHHHHQEHQL Hx₃H position not certain
                                                   (SEQ ID NO: 145)
ZCCT-Hb(Fan)     MSMACGLCGASNCPYHMMSPVLHHHHHHQEHR  Hx₃H position not certain
                                                   (SEQ ID NO: 146)
ZCCT-Ha          MSMSCGLCGASNCYHMMSPVL HHHHHQEHL  Hx₃H position not certain
                                                   (SEQ ID NO: 147)
ZCCT2_Td_B       MSMSCGLCGASNCPHHMISPVLQHHHHQEHRL Hx₃H position not certain
                                                   (SEQ ID NO: 148)
ZCCT2_DV92       MSMSCGLCGASDCPHHMISPVLQHQEQHWLREY   (SEQ ID NO: 149)
ZCCT2_Td_A       MSMSCGLCGASDCPHHMISPVLQHQEQHRLREY   (SEQ ID NO: 150)
```

***CO*-LIKE GROUP IV** (Yellow highlight: similar *ZCCT*)

```
OsI (SEQ ID NO: 151) MGMANEESPNYQVKKGGRIPPRSSLIYPFMSMGPAAGEGCGLCGADGGGCCSRHRHD
OsH (SEQ ID NO: 152)                          MSAASGAACGVCGGGVGECGCLLHQRRG
```

***CO*-LIKE Group I, II, III**

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HvCO1 (SEQ ID NO: 153)    MNCVSNGTVYEEAVGREGRWARLCDGCCTVPSVVYCRADSAYLCASCDA
HvCO3 (SEQ ID NO: 154) MIKAEPDLRGQLRGSAGVGGMQLQQRCDSCRSAPCAFYCRADSAALCAACDA
HvCO4 (SEQ ID NO: 155)    MEGEEKPVVGGAYWGVGARACDSCATEAARLFCRADAAFLCAGCDA
      (SEQ ID NO: 156)            RAHGSGSRHARVWLCEVCEHAPAAVTCKADAAVLCASCDA
OsJ   (SEQ ID NO: 157)       MASAAAATGAALGARTARACDGCMRRRARWHCPADDAFLCQACDA
OsN   (SEQ ID NO: 158)   MDALCDFCREQRSMVYCRSDAASLCLSCDRNVHSANALSRRHTRTLLCDRCVGQ
      (SEQ ID NO: 159)         PAAVRCLEENTSLCQNCDWNGHGAASSAAGHKRQTINCYSGCP
```